



1 GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTGTCTGCTCGCCGCTG 60
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGTAAGTACGAGCGACCCGAAAGAGAGACACCGCACCAAGAGACGAGCGCGGAC
M H S L G F F S V A C S L L A A A -
CGCTGCTCCCGGGTCTCGCGAGGCGCCCGCCCGCCCGCCCTTCGAGTCCGGACTCG 120
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGGCCAGGAGCGCTCCGCGGGCGGGCGGGCGGGAAGCTCAGGCCTGAGC
L L P G P R E A P A A A A A F E S G L D -
ACCTCTCGGACGCGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAGATCTGG 180
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTCTAGACC
L S D A E P D A G E A T A Y A S K D L E -
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACATCATGACTGTACTCTACCCAGAAT 240
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCCCTCGTCAATGCCAGACACAGGTACATCTACTTGAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y -
ATTGGAAAATGTACAAGTGTACGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG 300
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCCTTTCCCTCCGACCGTTGTAATTGTCTCTGTGTC
W K M Y K C Q L R K G G W Q H N R E Q A -
CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTGTGCTGCAGCACATTATAATACAG

FIG. 1A

301 -----+-----+-----+-----+-----+-----+-----+ 360
GGTGGAGTTGAGTTCCTGTCTTCTCTGATATTTAAACGACGTCGTGTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E -
361 AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT 420
-----+-----+-----+-----+-----+-----+-----+
TCTAGAACTTTTCATAAATACTATTAACCTCTTTCTGTAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C -
421 GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG 480
-----+-----+-----+-----+-----+-----+-----+
CATATCTACACCCCTTCCCTCAAACCTCAGCGCTGTTGTGGAAGAAATTTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V -
481 TGTCCGTCTACAGATGTGGGGTGTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 540
-----+-----+-----+-----+-----+-----+-----+
ACAGGCAGATGTCTACACCCCCCAACGACGTTATCACTCCCCGACGTCACGTAATTGTGGT
S V Y R C G C C C N S E G L Q C M N T S -
541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCTCTCTCAAGGCCCA 600
-----+-----+-----+-----+-----+-----+-----+
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCGGGGT
T S Y L S K T L F E I T V P L S Q G P K -
601 AACCAGTAACAATCAGTTTGGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG 660
-----+-----+-----+-----+-----+-----+-----+
TTGGTCATTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC
P V T I S F A N H T S C R C M S K L D V -

FIG. 1B

TTTACAGACAAAGTTCAATTCATATATAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720
-----+-----+-----+-----+-----+-----+
AAATGTCTCTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTCAACAG
Y R Q V H S I I R R S L P A T L P Q C Q -
AGGACGGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780
-----+-----+-----+-----+-----+-----+
TCCGTCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATAGTGTAGACGTCCTACGG
A A N K T C P T N Y M W N N H I C R C L -
TGGCTCAGGAAGATTTTATGTTTCCCTCGGATGCTGGAGATGACTCAACAGATGGATCC 840
-----+-----+-----+-----+-----+-----+
ACCGAGTCCCTTCTAAATAACAAAGGAGCCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D D S T D G F H -
ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTCAGTGTCTGCAGAG 900
-----+-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCCTC
D I C G P N K E L D E E T C Q C V C R A -
CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT 960
-----+-----+-----+-----+-----+-----+
GCCCCGAAGCCGGACGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C -
GTGTCTGTAAACAACACTCTTCCCCAGCCCAATGTGGGGCCAACCGAGAAATTGATGAAA 1020
-----+-----+-----+-----+-----+-----+
CACAGACATTTTGTGTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT

FIG. 1C

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V C K N K L F P S Q C G A N R E F D E N -
ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080
-----+-----+-----+-----+-----+-----+-----+
TGTGTACGGTCACACATACATTTCTTGGACGGGCTTTAGTTGGGGATTTAGGACCTT
T C Q C V C K R T C P R N Q P L N P G K -
AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC 1140
-----+-----+-----+-----+-----+-----+-----+
TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTCTTCAAGG
C A C E C T E S P Q K C L L K G K K F H -
ACCACCAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAGGCTTGTGAGC 1200
-----+-----+-----+-----+-----+-----+-----+
TGGTGGTTTGTACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
H Q T C S C Y R R P C T N R Q K A C E P -
CAGGATTTTCATATAGTGAAGAAAGTGTGTCGTTGTGTCCTTTCATATTTGGCAAGACCAC 1260
-----+-----+-----+-----+-----+-----+-----+
GTCCTAAAGTATATCACTTCTTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
G F S Y S E E V C C R C V P S Y W Q R P Q -
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAACCTGTGT
```

FIG. 1D

1261 -----+-----+-----+-----+-----+-----+-----+ 1320
TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
M S *
TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTTGGTCCATGCTAACAAAGACA 1380
1321 -----+-----+-----+-----+-----+-----+-----+
ACGGTGTCACTTTGACAGACACTTGTCTCTCTCTGGGAACACCCAGGTACGATGTGTTCTGT
AAAGTCTGTCTTTCCCTGAACCAATGTGGATAAATTTACAGAAATGGACTGGAGCTCATCTG 1440
1381 -----+-----+-----+-----+-----+-----+-----+
TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC
CAAAAGGCCCTCTGTAAAGACTGTGTTTCTGCCCAATGACCAACAGCCAAAGATTTTCCTC 1500
1441 -----+-----+-----+-----+-----+-----+-----+
GTTTTCGGAGAACATTTCTGACCAAAAGACGGTTACTGTTTGTCTGGTCTCTAAAAGGAG
TTGTGATTTCTTTAAAGAATGACTATATAATTTATTTCCACTAAAAATATGTTTCTGC 1560
1501 -----+-----+-----+-----+-----+-----+-----+
AACACTAAAGAAATTTCTTACTGATATATAATTAATAAAGGTGATTTTATATAACAAGACG
ATTCATTTTATAGCAACAACAATTGGTAAACTCACTGTGATCAATATTTTATATCAT 1620
1561 -----+-----+-----+-----+-----+-----+-----+
TAAGTAAATAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAAATATAGTA
GCAAAATATGTTTAAATAAATAATGAAAAATTGTATTTATAAAAAAATAAAAAA 1674
1621 -----+-----+-----+-----+-----+-----+-----+
CGTTTATACAAAATTTTATTTTACTTTTAAACATAAATAATTTTATTTTATTTT

FIG.1E

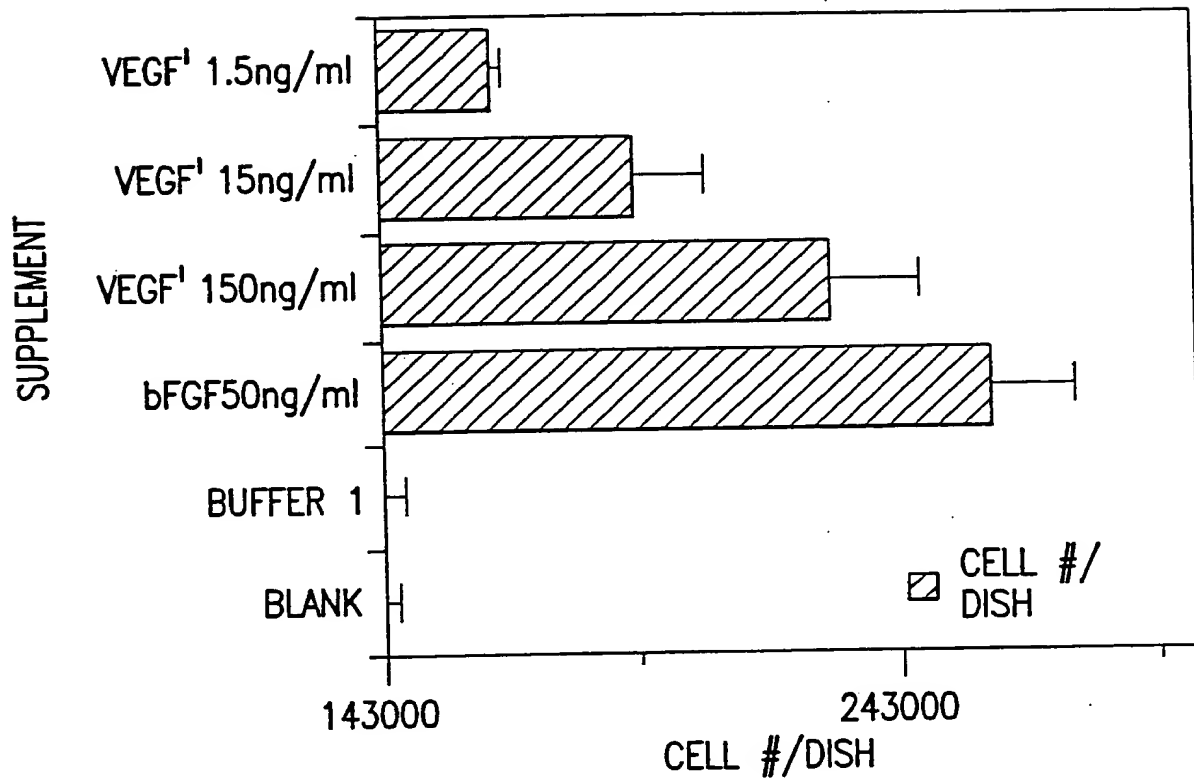


FIG.12

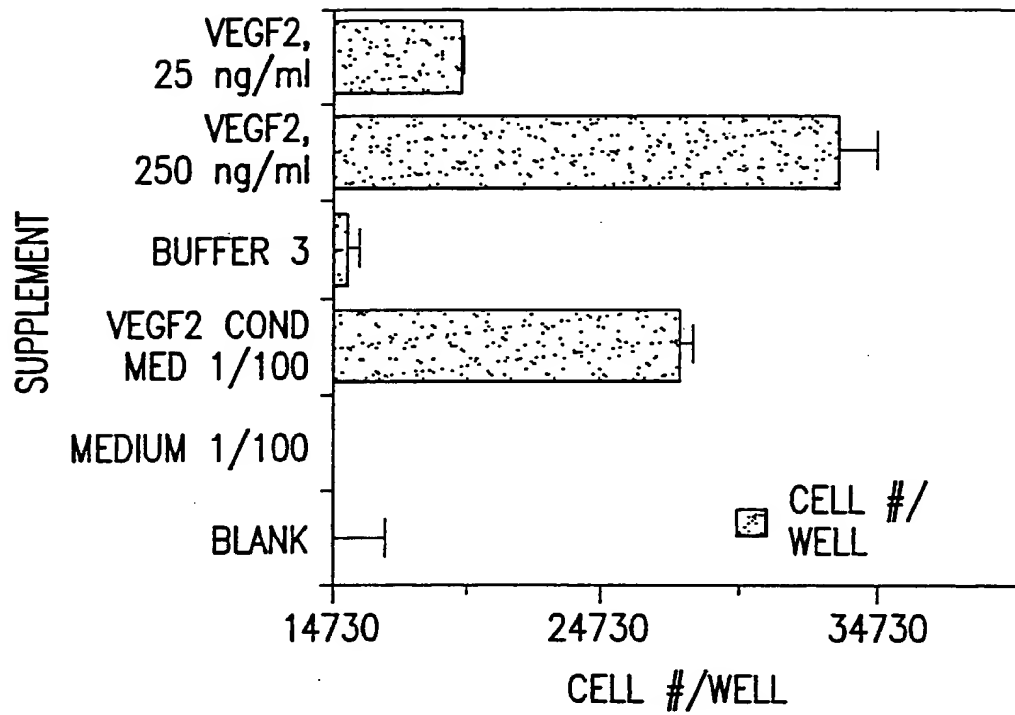


FIG.13